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1638

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MAY 2002

RAW SEQUENCE LISTING

DATE: 02/25/2002

PATENT APPLICATION: US/09/026,400A

TIME: 13:42:15

Input Set : A:\2185-226.app

Output Set: N:\CRF3\02252002\I026400A.raw

3 <110> APPLICANT: MORI, Satoshi
 4 NAKANISHI, Hiromi
 5 TAKAHASHI, Michiko
 7 <120> TITLE OF INVENTION: Nicotianamine Aminotransferase and Gene Therefor
 9 <130> FILE REFERENCE: 2185-0226P
 11 <140> CURRENT APPLICATION NUMBER: 09/026,400A
 C--> 12 <141> CURRENT FILING DATE: 2002-01-31
 14 <150> PRIOR APPLICATION NUMBER: 09-037499 JAPAN
 15 <151> PRIOR FILING DATE: 1997-02-21
 17 <160> NUMBER OF SEQ ID NOS: 7
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1660
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Hordeum vulgare
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (62)..(1444)
 30 <400> SEQUENCE: 1
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 33 a atg gta cac cag agc aac ggc cac ggc gag gcc gcc gcc gcc 109
 34 Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala
 35 1 5 10 15
 37 aac ggc aag agc aac ggg cac gcc gcc gcg aac ggc aag agc aac 157
 38 Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Ser Asn
 39 20 25 30
 41 ggg cac gcg gcg gcg gtg gag tgg aat ttc gcc cgg ggc aag 205
 42 Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
 43 35 40 45
 45 gac ggc atc ctg gcg acg acg ggg gcg aag aac agc atc cgg gcg ata 253
 46 Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
 47 50 55 60
 49 cgg tac aag atc agc gcg acg gtg gag gag agc ggg cgg ccc gtc 301
 50 Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
 51 65 70 75 80
 53 ctg ccg ctg gcc cac ggt gac ccg tcc gtg ttc ccg gcc ttc cgc acg 349
 54 Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
 55 85 90 95
 57 gcc gtc gag gcc gaa gac gcc gtc gcc gcc gcg ctg cgc acc ggc cag 397
 58 Ala Val Glu Ala Glu Asp Ala Val Ala Ala Leu Arg Thr Gly Gln
 59 100 105 110
 61 ttc aac tgc tac gcc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc 445
 62 Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala

Input Set : A:\2185-226.app
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63	115	120	125	
65	gta gca gag cac ttg tca cag ggc gtg ccc tac aag cta tcg gcc gac			493
66	Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp			
67	130	135	140	
69	gac gtc ttc ctc acc gcc ggc gga act cag gcg atc gaa gtc ata atc			541
70	Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile			
71	145	150	155	160
73	ccg gtg ctg gcc cag act gcc ggc aac ata ctg ctt ccc cgg cca			589
74	Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro			
75	165	170	175	
77	ggc tat cca aat tac gag ggc cga gca ttc aac aag ctg gag gtc			637
78	Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val			
79	180	185	190	
81	cgg cac ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac			685
82	Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp			
83	195	200	205	
85	tcg ctg gaa tcc atc gcc gac aag aac acc acc gcg atg gtc atc ata			733
86	Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile			
87	210	215	220	
89	aac cca aac aat ccg tgc ggc agc gtt tac tcc tac gac cat ctg gcc			781
90	Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala			
91	225	230	235	240
93	aag gtc gcg gag gtg gca agg aag ctc gga ata ttg gtg atc gct gac			829
94	Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp			
95	245	250	255	
97	gag gtt tac ggc aaa ctg gtt ctg ggc agc gcc ccg ttt atc ccg atg			877
98	Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met			
99	260	265	270	
101	ggc gtc ttt ggg cac att gcc ccg gtc ttg tcc att gga tct ctg tcc			925
102	Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser			
103	275	280	285	
105	aag tcg tgg ata gtg cct gga tgg cga ctt gga tgg gtg gcg gtg tac			973
106	Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr			
107	290	295	300	
109	gac ccc aca aag att tta gag aaa act aag atc tct acg tct att acg			1021
110	Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr			
111	305	310	315	320
113	aat tac ctt aat gtc tca acg gac cca gca acc ttc gtt cag gaa gct			1069
114	Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala			
115	325	330	335	
117	ctt cct aaa att ctt gag aac aca aaa gca gat ttc ttt aag agg att			1117
118	Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile			
119	340	345	350	
121	att ggt cta cta aag gaa tca tca gag ata tgt tat agg gaa ata aag			1165
122	Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys			
123	355	360	365	
125	gaa aac aaa tat att acg tgt cct cac aag cca gaa gga tcg atg ttt			1213
126	Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe			
127	370	375	380	

Input Set : A:\2185-226.app
Output Set: N:\CRF3\02252002\I026400A.raw

129 gta atg gtc aaa cta aac tta cat ctt ttg gag gag atc cat gac gac 1261
130 Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
131 385 390 395 400
133 ata gat ttt tgc tgc aag ctc gca aag gaa gaa tca gta att tta tgt 1309
134 Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
135 405 410 415
137 cca ggg agt gtt ctt gga atg gaa aat tgg gtc cgt att act ttt gcc 1357
138 Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
139 420 425 430
141 tgc gtt cca tct tct ctt caa gat gga ctc gaa agg gtc aaa tca ttc 1405
142 Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
143 435 440 445
145 tgt caa agg aac aag aag aag aat tct ata aat ggt tgt tagtgtaca 1454
146 Cys Gln Arg Asn Lys Lys Asn Ser Ile Asn Gly Cys
147 450 455 460
149 cacccctagt tgtacatctg actgaagctg taaatcattt ctatgttatcc cccattata 1514
151 tatttcaata aaacatattt gatatggttct gttgttagctg tccaagtcat gtactctact 1574
153 ttttgatgtt tttggcctca ttgccttgca tcaatttcaa taaaaatggt tgtgtacacc 1634
155 aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 1660
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159 <211> LENGTH: 461
160 <212> TYPE: PRT
161 <213> ORGANISM: Hordeum vulgare
163 <400> SEQUENCE: 2
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167 Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
168 20 25 30
170 Gly His Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
171 35 40 45
173 Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
174 50 55 60
176 Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
177 65 70 75 80
179 Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
180 85 90 95
182 Ala Val Glu Ala Glu Asp Ala Val Ala Ala Leu Arg Thr Gly Gln
183 100 105 110
185 Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
186 115 120 125
188 Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp
189 130 135 140
191 Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
192 145 150 155 160
194 Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
195 165 170 175
197 Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
198 180 185 190
200 Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp

Input Set : A:\2185-226.app
Output Set: N:\CRF3\02252002\I026400A.raw

201 195 200 205
203 Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile
204 210 215 220
206 Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
207 225 230 235 240
209 Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
210 245 250 255
212 Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
213 260 265 270
215 Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
216 275 280 285
218 Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
219 290 295 300
221 Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
222 305 310 315 320
224 Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala
225 325 330 335
227 Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
228 340 345 350
230 Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
231 355 360 365
233 Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
234 370 375 380
236 Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
237 385 390 395 400
239 Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
240 405 410 415
242 Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
243 420 425 430
245 Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
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253 <211> LENGTH: 1910
254 <212> TYPE: DNA
255 <213> ORGANISM: Hordeum vulgare
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (76)..(1728)
261 <400> SEQUENCE: 3
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265 Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala
266 1 5 10
268 aac ggc ctt gcc gtg gcc gca gcc gcg aac ggc aag agc aac ggc cat 159
269 Asn Gly Leu Ala Val Ala Ala Ala Asn Gly Lys Ser Asn Gly His
270 15 20 25
272 ggc gtg gct gcc gtg aac ggc aag agc aac ggc cat ggc gtg gat 207

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273	Gly	Val	Ala	Ala	Ala	Val	Asn	Gly	Ser	Asn	Gly	His	Gly	Val	Asp		
274	30					35					40						
276	gcc	gac	gcg	aac	ggc	aag	agc	aac	ggc	cat	ggc	gtg	gct	gcc	gac	gcg	255
277	Ala	Asp	Ala	Asn	Gly	Lys	Ser	Asn	Gly	His	Gly	Val	Ala	Ala	Asp	Ala	
278	45					50					55				60		
280	aac	ggc	aag	agc	aac	ggc	cat	gcc	gag	gcc	act	gcg	aac	ggc	cac	ggc	303
281	Asn	Gly	Lys	Ser	Asn	Gly	His	Ala	Glu	Ala	Thr	Ala	Asn	Gly	His	Gly	
282						65				70			75				
284	gag	gcc	act	gcg	aac	ggc	aag	acc	aac	ggc	cac	cgc	gag	agc	aac	ggc	351
285	Glu	Ala	Thr	Ala	Asn	Gly	Lys	Thr	Asn	Gly	His	Arg	Glu	Ser	Asn	Gly	
286						80			85			90					
288	cat	gct	gag	gcc	gcc	gac	gcg	aac	ggc	gag	agc	aac	gag	cat	gcc	gag	399
289	His	Ala	Glu	Ala	Ala	Asp	Ala	Asn	Gly	Glu	Ser	Asn	Glu	His	Ala	Glu	
290						95			100			105					
292	gac	tcc	gcg	gcg	aac	ggc	gag	agc	aac	ggg	cat	gcf	gcf	gcf	gcf	gca	447
293	Asp	Ser	Ala	Ala	Asn	Gly	Glu	Ser	Asn	Gly	His	Ala	Ala	Ala	Ala	Ala	
294						110			115			120					
296	gag	gag	gag	gag	gag	gtg	gag	tgg	aat	ttc	gcf	ggt	gcc	aag	gac	ggc	495
297	Glu	Glu	Glu	Glu	Ala	Val	Glu	Trp	Asn	Phe	Ala	Gly	Ala	Lys	Asp	Gly	
298	125					130					135			140			
300	gtg	ctg	gcg	gcg	acg	ggg	gcf	aac	atg	agc	atc	cgg	gcf	ata	cgg	tac	543
301	Val	Leu	Ala	Ala	Thr	Gly	Ala	Asn	Met	Ser	Ile	Arg	Ala	Ile	Arg	Tyr	
302						145				150			155				
304	aag	atc	agc	gcg	agc	gtg	cag	gag	aag	ggg	ccg	ccg	ccc	gtg	ctg	ccg	591
305	Lys	Ile	Ser	Ala	Ser	Val	Gln	Glu	Lys	Gly	Pro	Arg	Pro	Val	Leu	Pro	
306						160			165			170					
308	ctg	gcc	cac	ggg	gac	ccg	tcc	gtg	ttc	ccg	gcc	ttc	ccg	acg	gcc	gtc	639
309	Leu	Ala	His	Gly	Asp	Pro	Ser	Val	Phe	Pro	Ala	Phe	Arg	Thr	Ala	Val	
310						175			180			185					
312	gag	gcc	gag	gac	gcc	gtc	gcc	gcc	gtg	ccg	acc	ggc	cag	ttc	aac		687
313	Glu	Ala	Glu	Asp	Ala	Val	Ala	Ala	Ala	Val	Arg	Thr	Gly	Gln	Phe	Asn	
314						190			195			200					
316	tgc	tac	ccc	gcc	ggc	gtc	ggc	ctc	ccc	gcc	gca	cga	agc	gcc	gtg	gca	735
317	Cys	Tyr	Pro	Ala	Gly	Val	Gly	Leu	Pro	Ala	Ala	Arg	Ser	Ala	Val	Ala	
318	205					210				215			220				
320	gag	cac	ctg	tcg	cag	ggc	gtg	ccg	tac	atg	cta	tcg	gcc	gac	gac	gtc	783
321	Glu	His	Leu	Ser	Gln	Gly	Val	Pro	Tyr	Met	Leu	Ser	Ala	Asp	Asp	Val	
322						225			230			235					
324	ttc	ctc	acc	gcc	ggg	acc	cag	gcg	atc	gag	gtc	ata	atc	ccg	gtg		831
325	Phe	Leu	Thr	Ala	Gly	Gly	Thr	Gln	Ala	Ile	Glu	Val	Ile	Ile	Pro	Val	
326						240			245			250					
328	ctg	gcc	cag	acc	gcc	ggc	aac	att	ctg	ctc	ccc	agg	cca	ggc	tac		879
329	Leu	Ala	Gln	Thr	Ala	Gly	Ala	Asn	Ile	Leu	Leu	Pro	Arg	Pro	Gly	Tyr	
330						255			260			265					
332	cca	aac	tac	gag	gcg	ccg	gcc	gcf	ttc	aac	agg	ctg	gag	gtc	ccg	cat	927
333	Pro	Asn	Tyr	Glu	Ala	Arg	Ala	Ala	Phe	Asn	Arg	Leu	Glu	Val	Arg	His	
334						270			275			280					
336	ttc	gac	ctc	atc	ccc	gac	aag	ggg	tgg	gag	atc	gac	atc	gac	tcg	ctg	975
337	Phe	Asp	Leu	Ile	Pro	Asp	Lys	Gly	Trp	Glu	Ile	Asp	Ile	Asp	Ser	Leu	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/026,400A

DATE: 02/25/2002
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Input Set : A:\2185-226.app
Output Set: N:\CRF3\02252002\I026400A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6